

**IN THE SPECIFICATION:**

**Pages 6, 7 and 8 lines 20-25 through Page 7, lines 1-30, and Page 8, lines 13-18:**

The present invention provides a method of producing a purified  $\alpha$ -N-acetylgalactosaminidase (SEQ ID No:1-16 10 and Figure 15 (SEQ ID No: 1)), and functional analogs thereof, from *Clostridium perfringens* which are free of neuraminidase activity. A detailed description of the isolation protocols and its properties are set forth in the Experimental Section.

By functional analogs, it is meant that an analog is generally at least 70% homologous over any portion that is functionally relevant. In more preferred embodiments the homology is at least 80% and can approach 95% homology to the  $\alpha$ -N-acetylgalactosaminidase. The amino acid sequence of an analog can differ from that of the  $\alpha$ -N-acetylgalactosaminidase when at least one residue is deleted, inserted or substituted. Differences in glycosylation can provide analogs. The molecular weight of the  $\alpha$ -N-acetylgalactosaminidase can vary between the analog and the present invention due to carbohydrate differences. For example, the following are the N-terminal and tryptic amino acid sequence data obtained from the purified enzyme. These sequences (SEQ ID Nos: 8-15 2-10) have a percent homology of at least 90%.

N-terminal sequence: (K)VLGNYIQRNFHYDGKSFYT(T)(S)FLN (SEQ ID No:8 2).

Internal Sequence (trypsin fragments):

EDGSVEVK (SEQ ID No:9 3);  
 ATVSLPR (SEQ ID No:10 4);  
 LPAA(F/I)RKA (SEQ ID No:11 5);  
 IILKEF (SEQ ID No:12 6);  
 DSQYYEFLIER (SEQ ID No:13 7);  
 (K)YDVVLGNK (SEQ ID No:14 8); and  
 (F)PNELK (SEQ ID No:15 9).

CNBr Cleavage: ANFNGYYVELGQPIYAKSL (SEQ ID NO.: ~~46~~ 10)

The *C. perfringens* orf 325 sequence is found at Table 2 5. The CPE0325 coding sequence starts at the ATG start codon at nucleotide 108014 and extends to the TAA stop codon at nucleotide 109903. This DNA sequence is part of GenBank accession number AP003186, which is section 2 of the complete genome sequence of *Clostridium perfringens* strain 13. The CPE0325 coding sequence is annotated as a hypothetical protein and no functional assignment for this protein is included in the annotation that accompanies this GenBank entry. Query of the complete genome sequence of *Clostridium perfringens* with the empirically determined N-terminal amino acid sequence of purified alpha-N-acetylgalactosaminidase resulted in a match (100% sequence identity) between the 25 residue peptide sequence and amino acids 2-26 of CPE0325. The 25 amino acid sequence was not present in any other deduced *C. perfringens* translation product (protein), nor any other protein sequence in the GenBank database. Furthermore, each of seven internal peptide sequences (determined by amino acid sequencing of tryptic peptides) can be identified within the CPE0325 ORF. These findings identify the CPE0325 hypothetical protein as the alpha-N-acetylgalactosaminidase of *C. perfringens*.

More specifically, the N-terminal sequence set forth above follows the Met start codon. The internal fragments are scattered. Sequence ID Numbers ~~9~~ 2, ~~13~~ 7, and ~~15~~ 9 are in the last 40 residues. Sequence ID Number ~~10~~ 4 is within the first 10 residues, Sequence ID Numbers ~~11~~ 4 and ~~12~~ 5 overlap and the best matches are at about residue 210, Sequence ID Number ~~14~~ 7 is at about 455.